AMENDMENTS TO THE CLAIMS

1.-37. (Canceled)

38. (Currently Amended) The method of claim 111 wherein ~~said~~ the nucleic acid target is RNA.

39. (Currently Amended) The method of claim 111 wherein ~~said~~ the nucleic acid target comprises RNA and one or more deoxynucleotides ~~at preselected locations~~.

40.-94. (Canceled)

95. (Currently Amended) The method of claim 111, wherein each ~~member of said mixture of compounds~~ test compound is an oligonucleotide.

96. (Canceled)

97. (Currently Amended) The method of claim 111, wherein each ~~member of said mixture of compounds~~ test compound is a small molecule.

98. (Currently Amended) The method of claim 38, wherein ~~said~~ the RNA comprises a molecular interaction site present in two or more distinct taxonomic species.

99. (Currently Amended) The method of claim 112, wherein each ~~member of said mixture of compounds~~ test compound is an oligonucleotide.

100. (Canceled)

101. (Currently Amended) The method of claim 112, wherein ~~said~~ the nucleic acid target is RNA.

102. (Canceled)

103.   (Currently Amended) The method of claim 101, wherein ~~said~~ the RNA comprises a molecular interaction site present in two or more distinct taxonomic species.

104.   (Currently Amended) The method of claim 112, wherein each ~~member of said mixture of compounds~~ test compound is a small molecule.

105.-108. (Canceled)

109.   (Currently Amended) The method of claim 38, wherein ~~said~~ the RNA comprises a molecular interaction site.

110.   (Currently Amended) The method of claim 101, wherein ~~said~~ the RNA comprises a molecular interaction site.

111.   (Currently Amended) A method comprising

    (a) selecting a nucleic acid target comprising at least one loop, bulge, kink, stem structure, or mismatched base pair, wherein the mass of the nucleic acid target is known;

    (b) forming a first complex comprising a standard binding compound and ~~said~~ the nucleic acid target~~, wherein the complex has a known ion abundance and mass to charge ratio~~;

    (c) combining ~~said~~ the first complex with a mixture of two or more test ~~known~~ compounds under competitive binding conditions to allow formation of at least one test compound-nucleic acid target complex, wherein the mass of each test compound is known;

    (d) subjecting ~~said~~ the combination of step (c) to mass spectrometry;

    (e) collecting mass spectral data for ~~said~~ the combination, wherein ~~said~~ the mass spectral data ~~provides~~ comprises an ion abundance and a mass to charge ratio for ~~a plurality of ions~~ an ion of at least one test compound-nucleic acid target complex;

    (f) calculating the mass of at least one test compound-nucleic acid target complex ~~comparing at least one mass to charge ratio obtained in step (e) to the known mass~~

to charge ratio of the complex to determine whether binding of one or more members of said mixture of known compounds to the nucleic acid target has occurred; and

(g) calculating the difference between the known mass of the nucleic acid target and said one or more members at least one test compound-nucleic acid target complex to determine the identity of the test compound bound in the at least one test compound-nucleic acid target complex said one or more members of said mixture of known compounds.

112. (Currently Amended) A method comprising

(a) forming a first complex of comprising a nucleic acid target and a standard binding compound, wherein the nucleic acid target comprises at least one loop, bulge, kink, stem structure, or mismatched base pair;

(b) subjecting said the first complex to mass spectrometry;

(c) collecting mass spectral data for said the first complex, wherein the mass spectral data provides comprises an ion abundance and a mass to charge ratio for an ion of the complex;

(d) combining said the first complex with a mixture of two or more test known compounds under competitive binding conditions to allow formation of at least one test compound-nucleic acid target complex, wherein the mass of each test compound is known;

(e) subjecting said the combination of step (c) (d) to mass spectrometry;

(f) collecting mass spectral data for said the combination, wherein said the mass spectral data provides comprises an ion abundance and a mass to charge ratio for one or more of a plurality of ions an ion of at least one test compound-nucleic acid target complex;

(g) calculating the mass for the first complex and for at least one test compound-nucleic acid target complex comparing the mass to charge ratio collected in steps (e) and (f), to determine whether binding of one or more members of the mixture of known compounds to the nucleic acid target has occurred; and

(h) calculating the difference between the mass of the first complex and at least one test compound-nucleic acid target complex said one or more members to

determine the identity of <u>the test compound bound in the at least one test compound-nucleic acid target complex</u> ~~said one or more members of said mixture of known compounds~~.

113 and 114 (cancelled)

115. (new) The method of claim 111, wherein the binding affinity of the standard binding compound for the nucleic acid target is known.

116. (new) The method of claim 115, comprising using the ion abundance data collected in step (e) to calculate the relative concentrations of the first complex and the at least one test compound-nucleic acid target complex.

117. (new) The method of claim 116 comprising calculating the binding affinity of the bound test compound for the nucleic acid target.

118. (new) The method of claim 112, wherein the binding affinity of the standard binding compound for the nucleic acid target is known.

119. (new) The method of claim 118, comprising using the ion abundance data collected in step (f) to calculate the relative concentrations of the first complex and the at least one test compound-nucleic acid target complex.

120. (new) The method of claim 119 comprising calculating the binding affinity of the bound test compound for the nucleic acid target.